GCCATCCCAT CAACAGAAGG TTTAAGTGGA AATCCATTTC ATTAGAAAAG 50

ATCGGACAAA GGGTACTCTT AAGCATACAA C ATG AGG GCG GTG GCG 96
                                  Met Arg Ala Val Ala
                                           5

GTT TTT GCT TGC GTT CTC TTC TGT ATG GTT CAC AAA GCC 138
Val Phe Ala Cys Val Leu Phe Cys Met Val His Lys Ala
              10   15

GCA CTT GCG GAT GAT AAA ACG TGC AAC CCT ACA GAT TTT ATG 180
Ala Leu Ala Asp Asp Lys Thr Cys Asn Pro Thr Asp Phe Met
           20   25   30

GTT ACC CAA ACC ATA ACT GGA TTG ACA ATC GGC GGT AAA CAA 222
Val Thr Gln Thr Ile Thr Gly Leu Thr Ile Gly Gly Lys Gln
           35   40   45

GAG TTC GAG GTC AAT TTA ATA AAC AAT TTG TAT TGT GCA CAA 264
Glu Phe Glu Val Asn Leu Ile Asn Asn Leu Tyr Cys Ala Gln
          50   55   60

A - A

FIG. 1a

A - - - - - - - - A

TCT AAT GTC AAA GTT TCA TGT GAC GGG CTT CAT ACC ACC GAA
Ser Asn Val Lys Val Ser Cys Asp Gly Leu His Thr Thr Glu
          65   70   75   306

CCA ATA GAT CCT CAC ATT ATC AGA CCA CTT AGT GAC GGA ACG
Pro Ile Asp Pro His Ile Ile Arg Pro Leu Ser Asp Gly Thr
              80   85   348

AAC AAC TGC CTT GTC AAC AAT GGA GCG CCT ATT TCT CAT GCT
Asn Asn Cys Leu Val Asn Asn Gly Ala Pro Ile Ser His Ala
      90   95   100   390

ACT CTT GTA GCA TTC AAG TAT GCC TGG GAT GTT CCT CCA TCT
Thr Leu Val Ala Phe Lys Tyr Ala Trp Asp Val Pro Pro Ser
         105   110   115   432

TTC AGC ATC ATC AGC TCT GAT ATA AAT TGC TCC TAA
Phe Ser Ile Ile Ser Ser Asp Ile Asn Cys Ser OCH
         120   125   468

GGAGAAA ATTCTAGTTG GCAGAGAATA ATCATATAGT CTTTTTTACT   515

B - - - - - - - - B

FIG. 1b

B --·--·--·--·--·--·--·--·--·--·-- B

GAGCTATTTA ATTTTTTCAA TTTTCACCAA TAAGATTATT TTAATGGAAT 565

GTTAATGTAT TAGAATTGAA AAATAAAAAA AAAAAAAAAA AAAAAAAAAA 615

AAAAAAAAAA 625

FIG. 1c

```
GAAAGTTGAA ACATCTCCAT CAAACTCTAG AGTCAGATTT CCCACAAG                48

ATG ATT TCA TCG GCA AAT AAC AAA GGC GCC GGC ACA AGC                 87
Met Ile Ser Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser
              5                      10

CGC CGC AAG CTC CGT TCT GAG AAG GCT GCA CTC CAG TTC                126
Arg Arg Lys Leu Arg Ser Glu Lys Ala Ala Leu Gln Phe
         15                   20                   25

TCC GTC AGT CGC GTC GAA TAC TCC CTC AAG AAG GGG CGC                165
Ser Val Ser Arg Val Glu Tyr Ser Leu Lys Lys Gly Arg
              30                   35

TAT TGC AGG CGC TTA GGC GCT ACG GCC CCC GTC TAC CTA                204
Tyr Cys Arg Arg Leu Gly Ala Thr Ala Pro Val Tyr Leu
         40              45                   50

GCC GCC GTC CTT GAA AAC CTC GTG GCC GAA GTG TTG GAC                243
Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu Asp
         55              60                   65
```

A - A

FIG. 5a

A - A

```
ATG GCG GCG AAC GTG ACA GAA GAA ACA TCC CCC ATT GTT      282
Met Ala Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val
                 70                      75

ATC AAA CCG AGG CAT ATT ATG CTT GCC CCC AGG AAT GAT      321
Ile Lys Pro Arg His Ile Met Leu Ala Pro Arg Asn Asp
         80                      85                90

GTA GAA GTT CAA GCT GTT TCA CGG TGT CAC CAT CTC          360
Val Glu Val Gln Ala Val Ser Arg Cys His His Leu
             95                     100

GGC ATC AGG TGT CGT CCC TAAAAACACGC AAAGAGCTGG           398
Gly Ile Arg Cys Arg Pro
105                 110

ACCGTCGCAA ACGCCGTTCC ACCTTTCAGC CGGATTAGTT CTTGATATTT   448

CATTCTATCA ATCTTGGTTA TGTGACTGTG ATTTTTCGTT TTGTGTTGAA   498
```

B - B

FIG. 5b

B ----------------------- B

CTAAGCCCCC TAATCTGGAT TTCTCGTTTT ATGTTGAACT AAGTCTGTGC   548

ACTCTTGAAG TAAAAAAAAA AAAAAAAAAA AAAAAAAA   587

FIG. 5c

GATCCCAAAT CATCA ATG ACG ATC CCC GAA AAG AAA TCC GTC   42
               Met Thr Ile Pro Glu Lys Lys Ser Val
               1   5

GCT CCG ATG GCC CGT ATG AAG CAT ACA GCC CGC ATG TCT   81
Ala Pro Met Ala Arg Met Lys His Thr Ala Arg Met Ser
10   15   20

ACC GGC GGT AAG GCT CCA CGC AAG CAG CTC GCC TCT AAG   120
Thr Gly Gly Lys Ala Pro Arg Lys Gln Leu Ala Ser Lys
25   30   35

GCT CTT CGC AAG GCG CCA CCA CCG ACC AAA GGA GTG   159
Ala Leu Arg Lys Ala Pro Pro Pro Thr Lys Gly Val
40   45

AAG CAG CCC ACC ACT ACC TCC GGA AAA TGG CGC TTC   198
Lys Gln Pro Thr Thr Thr Ser Gly Lys Trp Arg Phe
50   55   60

A --- --- --- --- --- --- --- --- --- --- --- --- --- A

FIG. 6a

A

GCG AGA TTT CAC AGG AAA CTG CCA TTC CAA GGG CTG GTG
Ala Arg Phe His Arg Lys Leu Pro Phe Gln Gly Leu Val
          65   70   237

AGG AAA ATC TGG CAG GAC TTG AAG ACA CAT CTG CGC TTC
Arg Lys Ile Trp Gln Asp Leu Lys Thr His Leu Arg Phe
      75   80   85   276

AAG AAC CAC TCG GTT CCT CCA CTT GAG GAG GTA ACT GAG
Lys Asn His Ser Val Pro Pro Leu Glu Glu Val Thr Glu
              90   95   100 315

GTT TAT CCT TGC CAA ACT ATT GGA GGA TGC TAT
Val Tyr Pro Cys Gln Thr Ile Gly Gly Cys Tyr
              105   348

TAGGATATTG AATTTGGATA ATGGTTTAAT TATCTGTTCT ACCTTTATGA   398

TCAAATTTCT GTGGCTCAGC GTTGTGTAAT TTGGGCAATC GAATTCTTAG   448

CTATATTGCC TCAAAAAAAA AAAAAAAAA AAAAAAA   485

A

FIG. 6b

GGAGGGTGTT GGAATTAGGT TTGCCTAGGG TTTGCCTAGG TTTAGAGAAA   50

TAGTCAAAAT TGTCCTATTC TATAGGCATG ATTTAGTAGT GAGTTAATTA   100

TCCTATAATT TCTCTTCTTG TATGCTCAAA TAACTGGTTC TTTAATGAAT   150

AGATAATTAA GTTTGTAGC AATTTCTTCC TCAAATTGAG TATCAACAAT   200

TGTTAGATTG CTTTGGTGAT TATATTTGAT ATAATTGTTT GTAAGAATGT   250

GTAGTGAAAA GATTGTGATT ATTCATTTCG TTGTTGGACG AATTGTTAGA   300

GCCCCATCGC TAATGCCTTA TAGTACTCGA AATATGTTGG GAATAGAAGA   350

TGAAAAATCC CATTCTTTGT AGTAGGAGTA AAAATTTGTC TTTTCATTAT   400

TCCATTGAAT GTTAACCACT TGCCATTCAT CTGACGGGGA TGGCAGAGTT   450

CCGACCATCT AGTGATCCGT GGGATATTGA TTTGGTGTG TCAATGAAAT   500

TGTGAGAACG GGCTTCTGGG AGAGAAAAGC CCTCTTGCCT CTGATATGAA   550

CACTGAGGCT GATTATGTTA ACGGATGGAG ATTTATCAGT GGCTGAATTT   600

GGGTGCTGTA GAGACAGAAT TTGAAAGTTC TAACAATAAA CCCTAATTCT   650

GAACTTGGGC GGGGCTGGGA TTTTACTCTT AACGTGAAGA GAGGCAAGAT   700

GAATTGACAG CTTGGAAGTC GATCCAGTAT TTGCAGCAGT CGTGACGAAT   750

A - - - - - - - - - - - - - - - - - A

FIG. 10a

A -- A

```
TGGTTGGACA GTTACATCGG TCAGAGAATG CGTTCTATAA ATTCCCCCAA   800
TGCGGCAGTG AAAATCCCAT CCCATCAACA GAAGTTTTAA GTGGAAACCC   850
ATTCCAATAG AGAAGATCGA ACAAAGGGTA TTTAAACATA CAAATGGGGG   900
CAGTGGGTGTT TCTTTTTGCT TGCGTTCTCT TCTGTATGGT TCACA        945
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FIG. 10b